

OIPE

RAW SEQUENCE LISTING

DATE: 09/12/2001

PATENT APPLICATION: US/09/824,322A

TIME: 17:10:02

Input Set : A:\ES.txt

Output Set: N:\CRF3\09122001\I824322A.raw

Does Not Comply
Correct Diskette Needed

3 <110> APPLICANT: Baker, Brenda
 4 Bennett, C. Frank
 5 Butler, Madeline M.
 6 Shanahan, William R.
 8 <120> TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS
 FACTOR-ALPHA (TNF-
 9 ALPHA) EXPRESSION
 11 <130> FILE REFERENCE: ISPH-0501
 13 <140> CURRENT APPLICATION NUMBER: US/09/824,322A
 14 <141> CURRENT FILING DATE: 2001-04-02
 16 <150> PRIOR APPLICATION NUMBER: US 09/313,932
 17 <151> PRIOR FILING DATE: 1999-05-18
 19 <150> PRIOR APPLICATION NUMBER: US 09/166,186
 20 <151> PRIOR FILING DATE: 1998-10-05
 22 <160> NUMBER OF SEQ ID NOS: 503

ERRORED SEQUENCES

6005 <210> SEQ ID NO: 498
 6006 <211> LENGTH: 20 19 shown
 6007 <212> TYPE: DNA
 6008 <213> ORGANISM: Artificial Sequence
 6010 <220> FEATURE:
 6011 <223> OTHER INFORMATION: Synthetic
 6013 <400> SEQUENCE: 498
 E--> 6014 ctgattagag agaggtccc 19
 6016 <210> SEQ ID NO: 499
 6017 <211> LENGTH: 20 18
 6018 <212> TYPE: DNA
 6019 <213> ORGANISM: Artificial Sequence
 6021 <220> FEATURE:
 6022 <223> OTHER INFORMATION: Synthetic
 6024 <400> SEQUENCE: 499
 E--> 6025 ctgattagag agaggtccc 18
 6060 <210> SEQ ID NO: 503
 6061 <211> LENGTH: 20
 6062 <212> TYPE: DNA
 6063 <213> ORGANISM: Artificial Sequence
 6065 <220> FEATURE:
 6066 <223> OTHER INFORMATION: Synthetic
 6068 <400> SEQUENCE: 503
 6069 tccgtcatcg ctctcaggg 20
 W--> 6070 ??
 W--> 6078 1
 E--> 6081 95
 W--> 6084 Error! Main Document Only.

<210> 118

<211> 20

<212> DNA

<213> Artificial Sequence

see item 1102 Ena Summary Sheet

<400> 118

cccttcattc tcaaggcaca

20

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/824,322A

DATE: 09/12/2001

TIME: 17:10:04

Input Set : A:\ES.txt

Output Set: N:\CRF3\09122001\I824322A.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:598 M:283 W: Missing Blank Line separator, <400> field identifier
L:682 M:283 W: Missing Blank Line separator, <220> field identifier
L:955 M:283 W: Missing Blank Line separator, <220> field identifier
L:1250 M:283 W: Missing Blank Line separator, <220> field identifier
L:1396 M:283 W: Missing Blank Line separator, <220> field identifier
L:1838 M:258 W: Mandatory Feature missing, <220> FEATURE: ←
L:1838 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2244 M:283 W: Missing Blank Line separator, <400> field identifier
L:6014 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:19 SEQ:498 ✓
L:6025 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:18 SEQ:499 ✓
L:6070 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:6078 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:503
L:6081 M:254 E: No. of Bases conflict, LENGTH:Input:95 Counted:20 SEQ:503
L:6084 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/824,322A |
|--|--|----------------------------|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE | | |
| 1 _____ Wrapped Nucleics Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." | |
| 2 _____ Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. | |
| 3 _____ Misaligned Amino Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. | |
| 4 _____ Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. | |
| 5 _____ Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. | |
| 6 _____ PatentIn 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. | |
| 7 _____ Skipped Sequences (OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. | |
| 8 _____ Skipped Sequences (NEW RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000 | |
| 9 _____ Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. | |
| 10 _____ Invalid <213> Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence | |
| 11 _____ Use of <220> | Sequence(s) <u>118</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) | |
| 12 _____ PatentIn 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. | |
| 13 _____ Misuse of n | n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide. | |